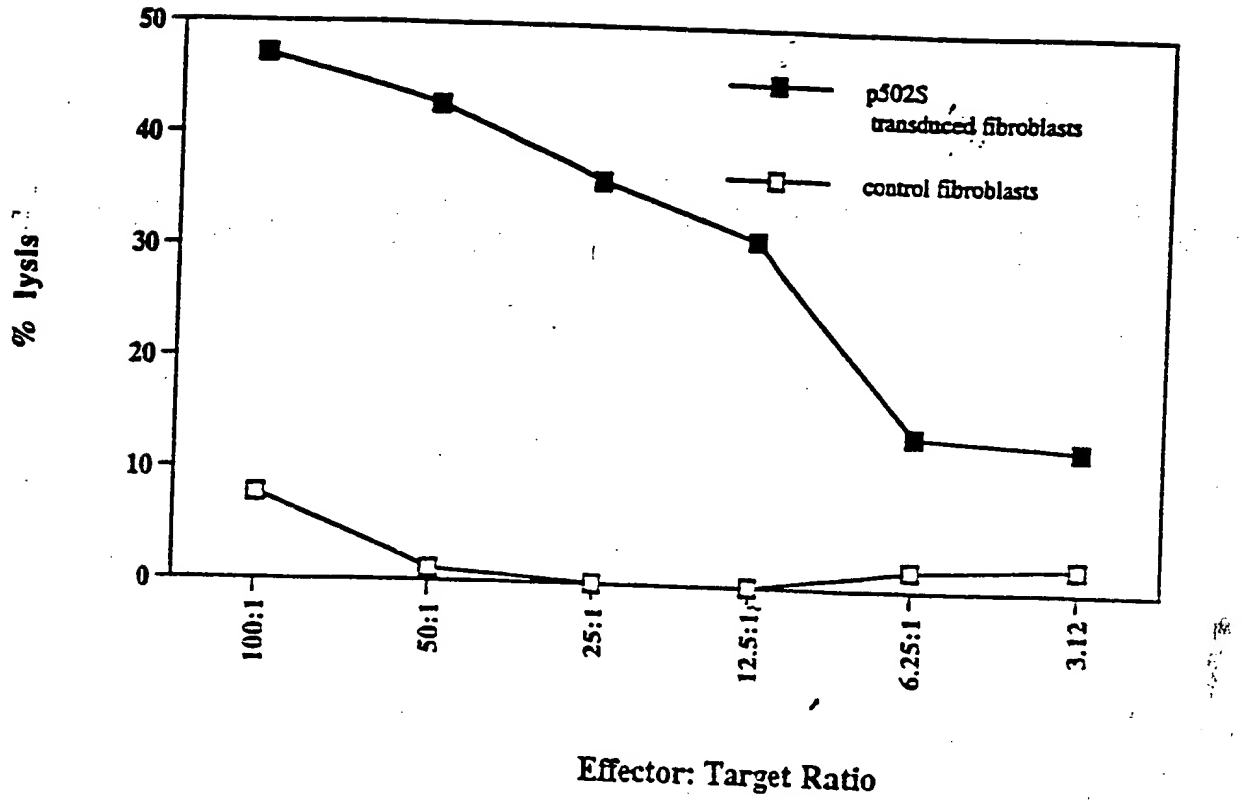

50
40
30
20
10
0
% lysis
p502S transduced fibroblasts
control fibroblasts
100:1
50:1
25:1
12.5:1
6.25:1
3.12
Effector: Target Ratio

FIG. 1

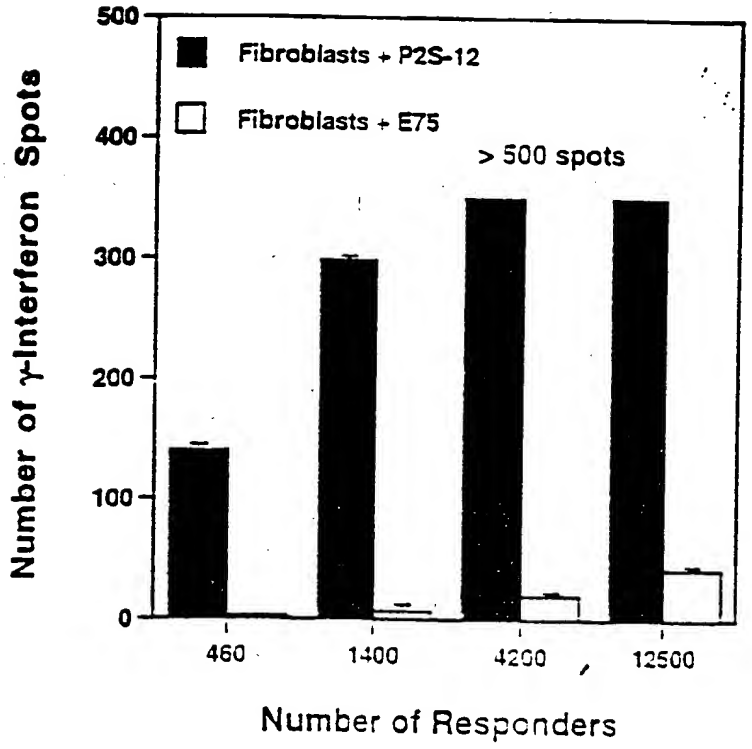

500
400
300
200
100
0
Number of γ-Interferon Spots
Fibroblasts + P2S-12
Fibroblasts + E75
> 500 spots
460
1400
4200
12500
Number of Responders

FIG. 2A

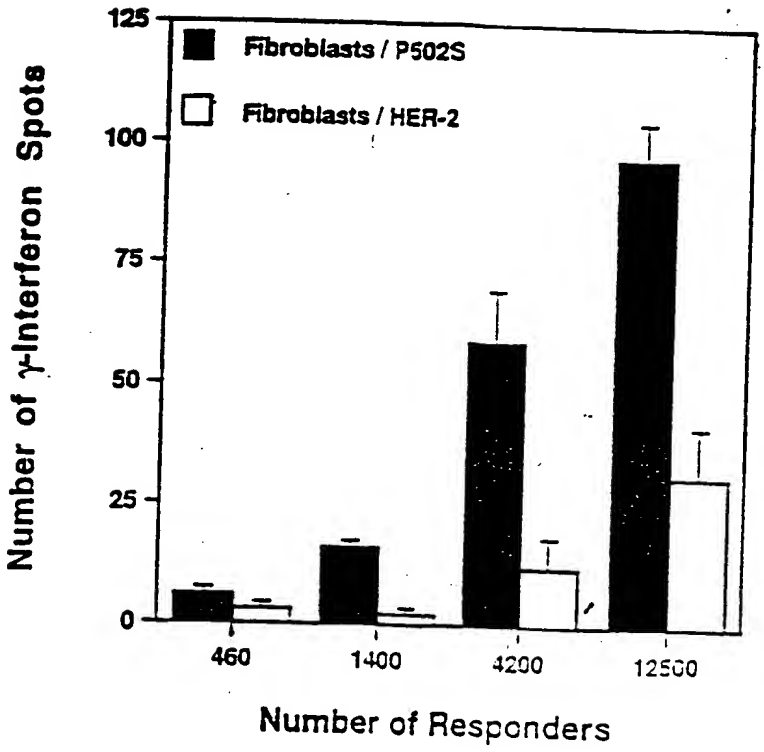

Fibroblasts / P502S
Fibroblasts / HER-2
Number of γ-Interferon Spots
125
100
75
50
25
0
460
1400
4200
12500
Number of Responders

FIG. 2B

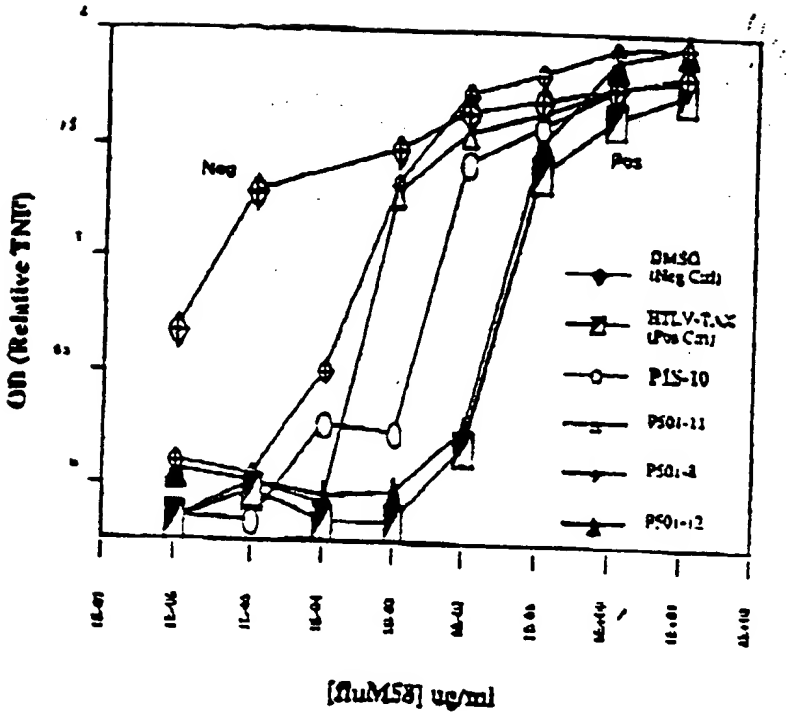

OD (Relative TNF)
Neg
Pos
DMSO
(Neg Ctrl)
HTLV-T.
(Pos Ctrl)
P1S-10
P501-11
P501-8
P501-12
[fluM58] ug/ml

Figure 3

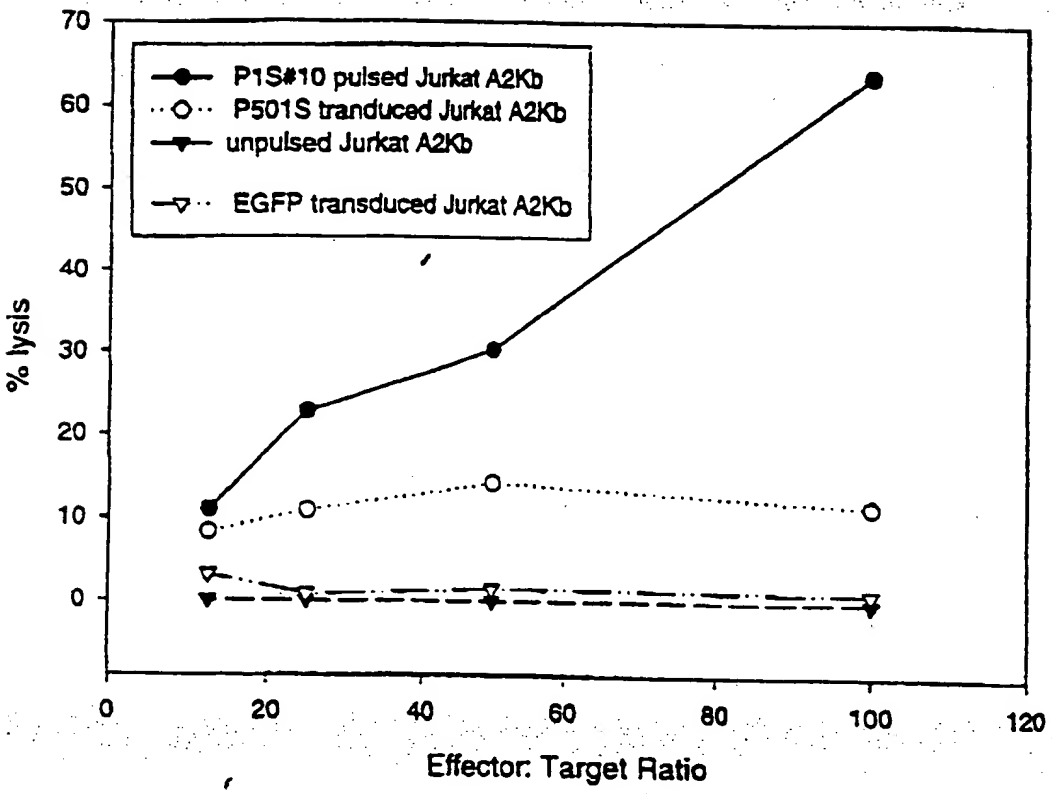

P1S#10 pulsed Jurkat A2Kb
P501S tranduced Jurkat A2Kb
unpulsed Jurkat A2Kb
EGFP transduced Jurkat A2Kb
% lysis
Effector: Target Ratio
0
10
20
30
40
50
60
70
0
20
40
60
80
100
120

Figure 4

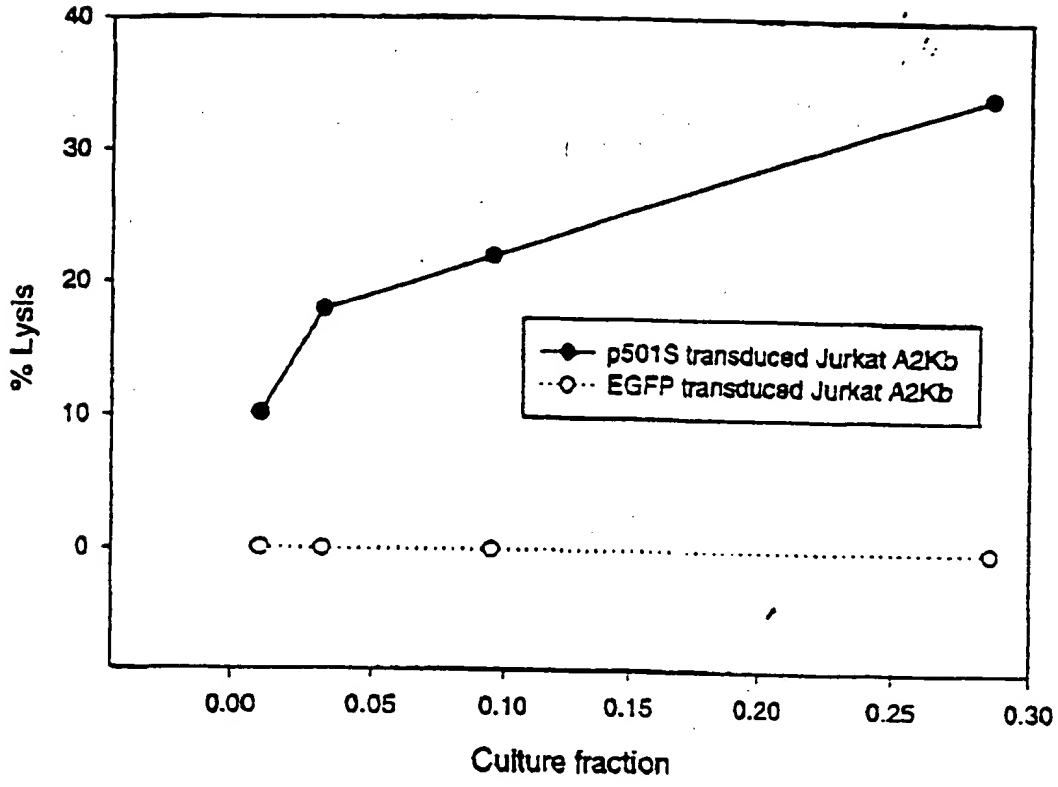

40
30
20
10
0
% Lysis
p501S transduced Jurkat A2Kb
EGFP transduced Jurkat A2Kb
0.00
0.05
0.10
0.15
0.20
0.25
0.30
Culture fraction

Figure 5

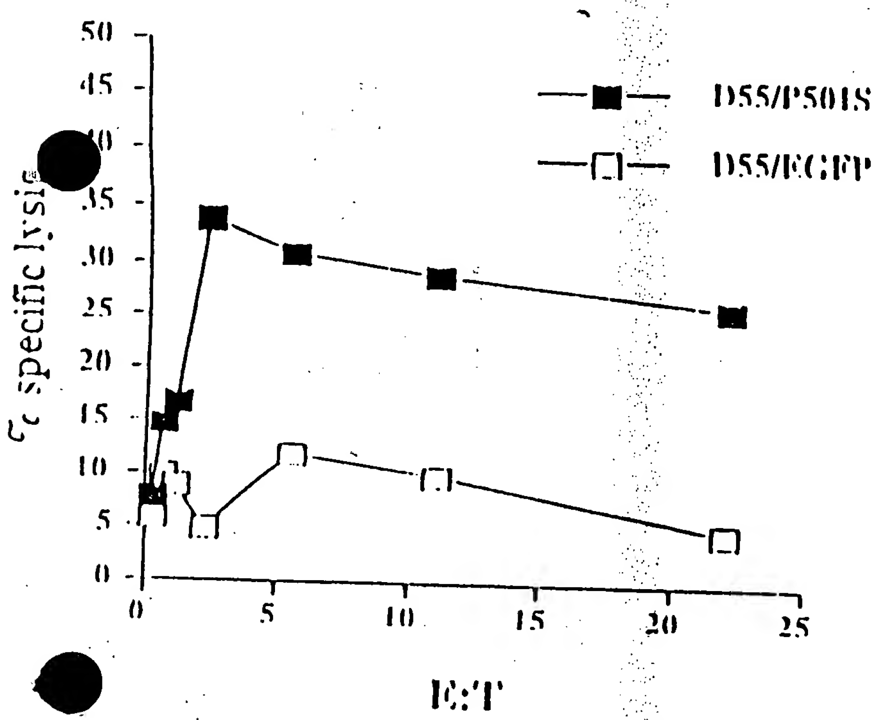


Fig. 6A

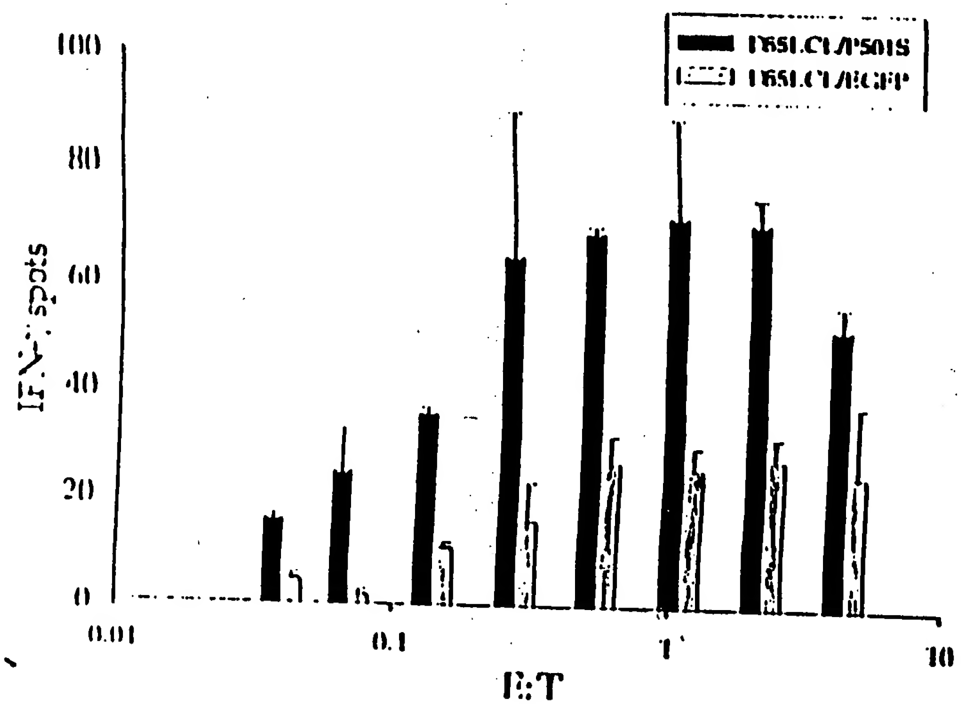
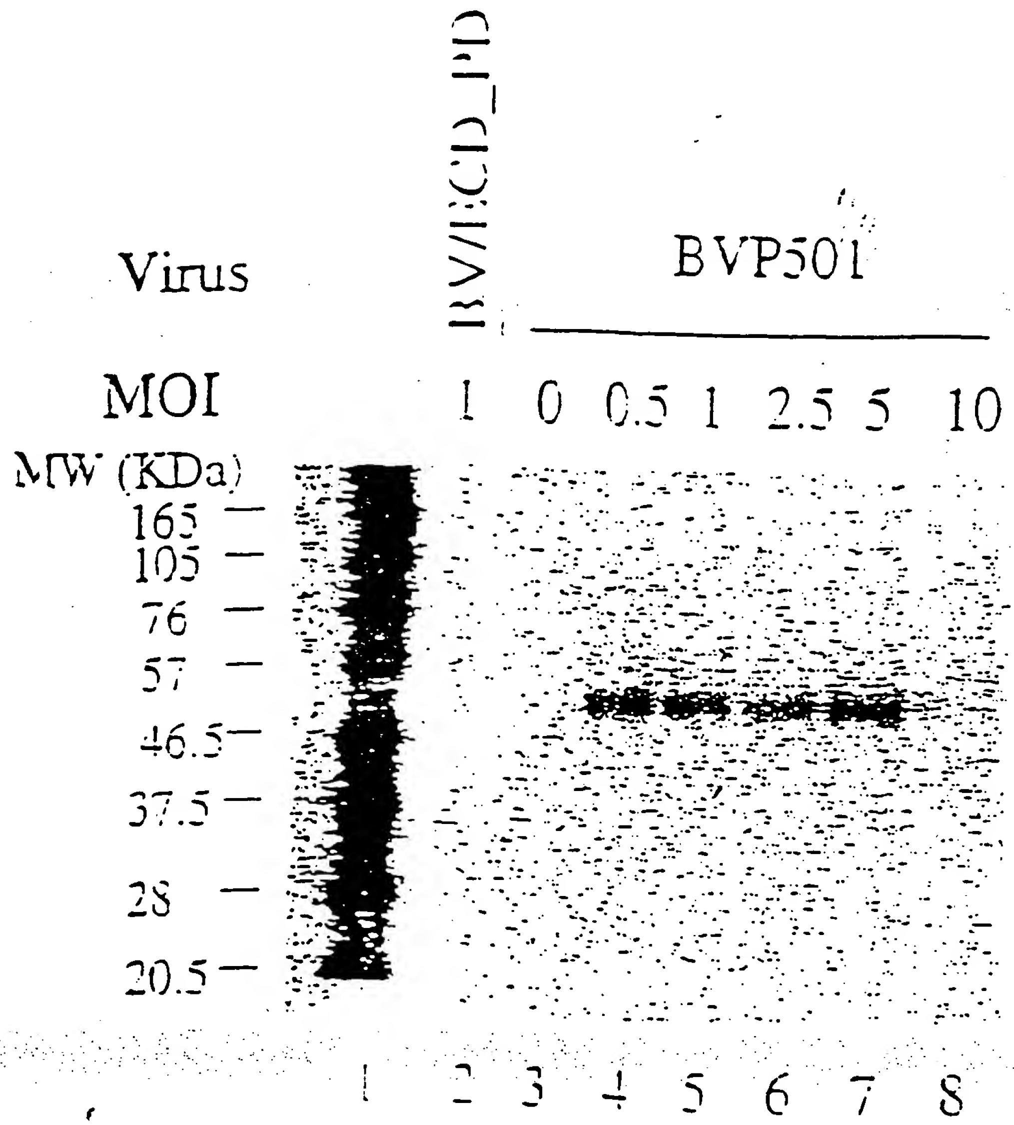


Fig. 6B

Expression of P501S by the Baculovirus Expression System



0.6 million high [illegible] 6-well plate were infected with an unrelated control virus BV/ECD_PD [illegible] without virus (lane 3), or with recombinant baculovirus for P501 at differ[illegible] (lane 4 - 8). Cell lysates were run on SDS-PAGE under the reducing [illegible] and analyzed by Western blot with a monoclonal antibody against [illegible] (P501S-10E3-G4D3). Lane 1 is the biotinylated protein molecular weight m[illegible] (BioLabs).

Fig. 7

Figure 8. Mapping of the epitope recognized by 10E3-G4-D3

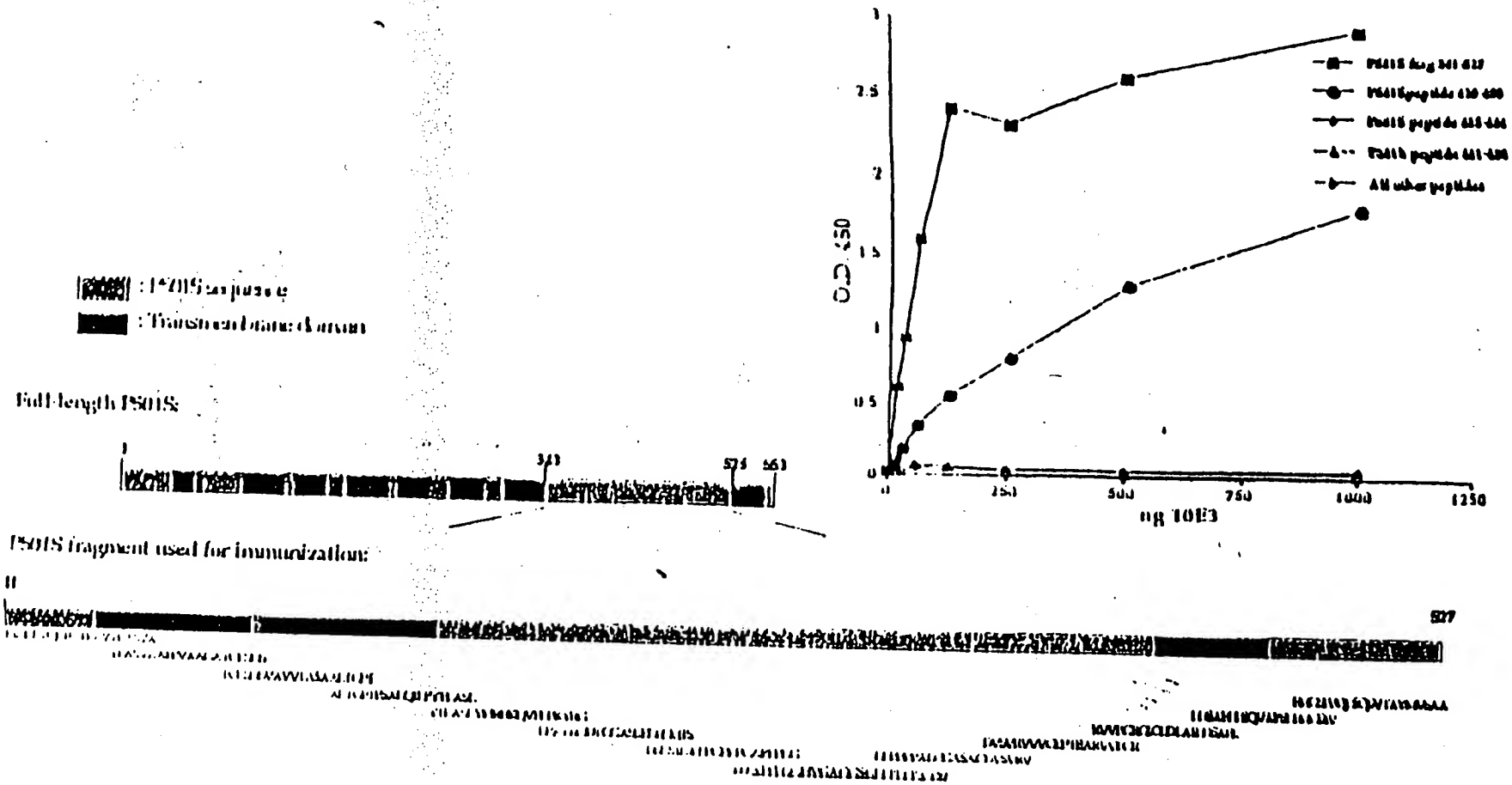


FIG 8

Figure 1. Schematic of P501S with predicted transmembrane, cytoplasmic, and extracellular regions

MVQRLAVVSRLLRHRK AQLLLVNLLTFGLEVCLAAGIT YVPPLLLRVGVEEKEM TMVLGIGPYLGLVCVPLLGSAS

DHWRGRYGRRRP FIWALSLGILLSLFLIPRAGWL AGLLCPDPRPLE LALLLLGVGLLDFCGQVCFTPL

EALLSDLFRDPDHCRQ AYSVYAFMISLGGCLGYLLPAL DWDTSALAPYLGTQIE

CLPGLATLIFLTCVAATLLY *AEEAALGPTEPAEGLSAPSLSPHCTPCRARLAFRNLGALLPRL*

HQLCCRAIPRTLRR LPVAFLCSWMALMTFTLFYTDP VGRGLYQGVPRAIPGTEARRHYDEGVR

MGSLGLFLQCAISLVFSLVM *DRLVQREGTRAVYLAS* VAAFPYAAGIATCLSHSVAVVTA *SAA*

LTGETFSALGILPYTLASLY *HREKQVFLPKYRGDTGGASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGL*

LPPPPALCGASACDVSVRVVVGEPTEARVVPGRG ICLDLAILDSAFLLSQVAPSLP MGSIVQLSQS

VTAYMVSAAGLGLVALYFAT *QVVFDKSDLAKYSA*

Underlined sequence: Predicted transmembrane domain; Bold sequence: Predicted extracellular domain; *Italic sequence*: Predicted intracellular domain. Sequence in bold/underlined: used to generate polyclonal rabbit serum

Localization of domains predicted using HMMTOP (G.E. Tusnady and I. Simon (1998) Principles Governing Amino Acid Composition of Integral Membrane Proteins: Applications to topology Prediction.J.Mol Biol. 283, 489-506.

Fig. 9

Genomic Map of (5) Corixa Candidate Genes

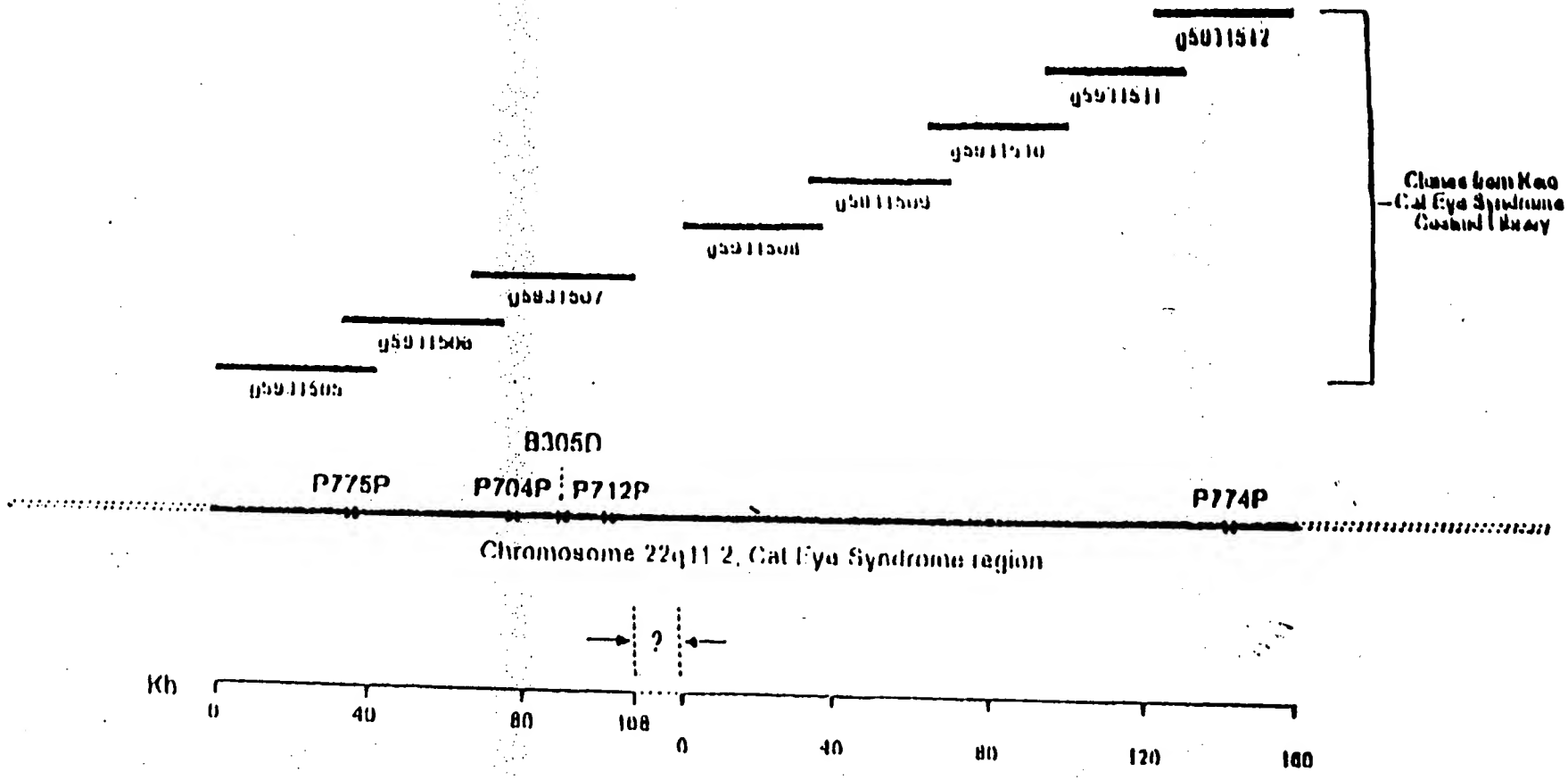


Fig. 10

FIGURE 4. Elisa assay of rabbit polyclonal antibody specificity

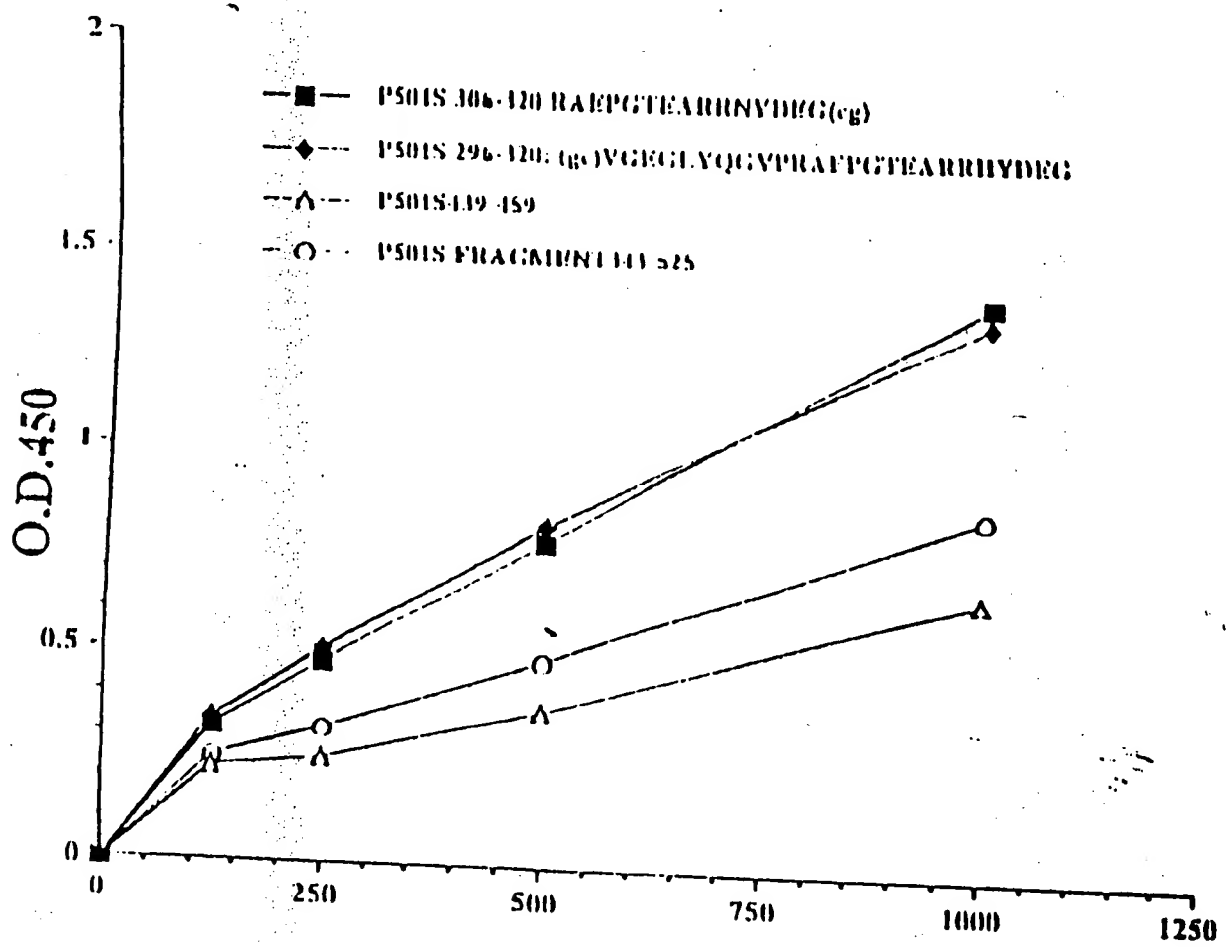
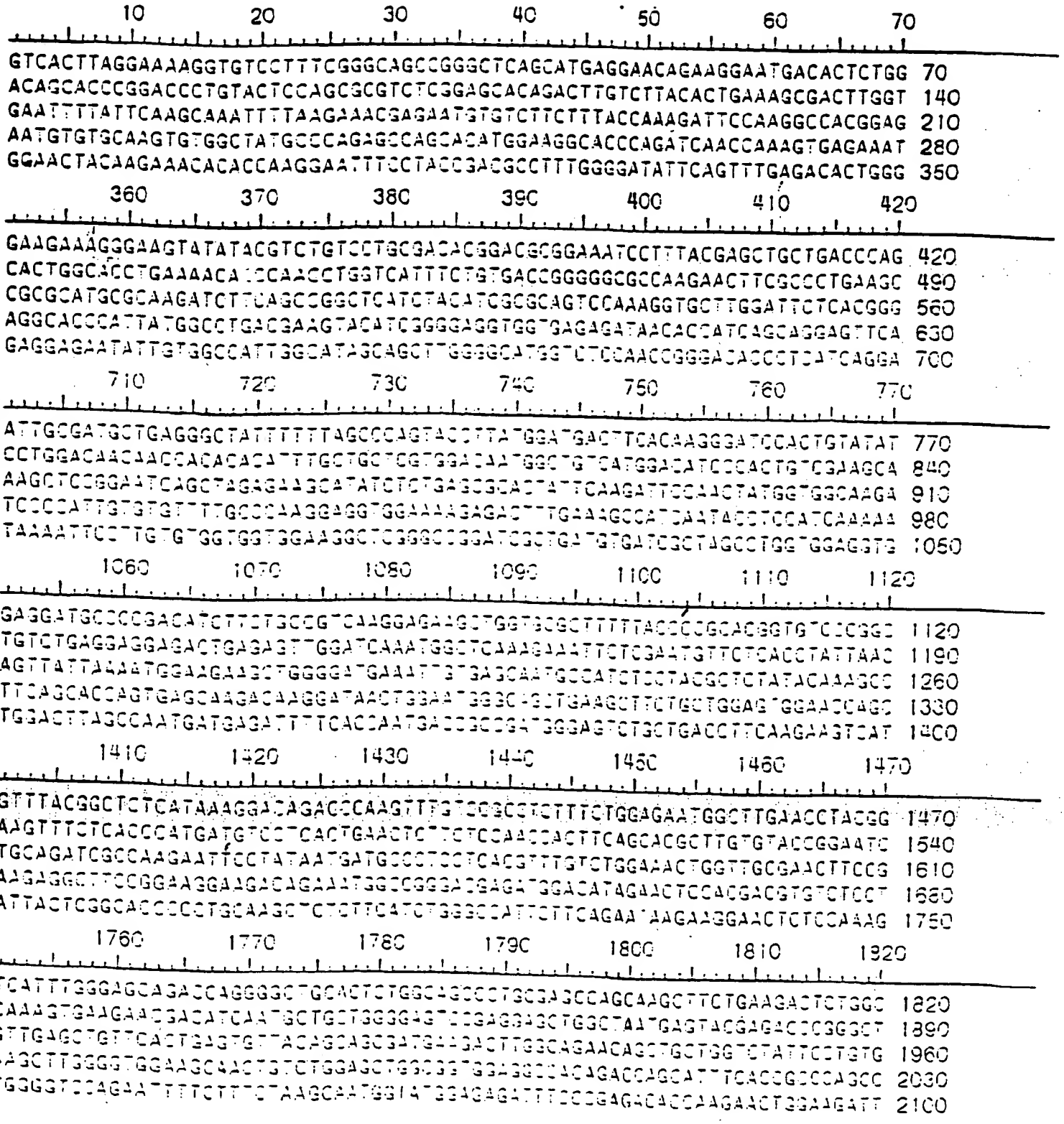


Fig. 11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AATGTGTGCAAGTGTGGCTATGCCCAGAGCCAGCACATGGAAGGCACCCAGATCAACCAAAGTGAGAAAT 280
GGAACTACAAGAAACACACCAAGGAATTTCCTACCGACGCCTTTGGGGATATTCAGTTTGAGACACTGGG 350
360 370 380 390 400 410 420
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CACTGGCACCTGAAAACA CCAACCTGGTCATTTCTGTGACCGGGGGCGCCAAGAACTTCGCCCTGAAGC 490
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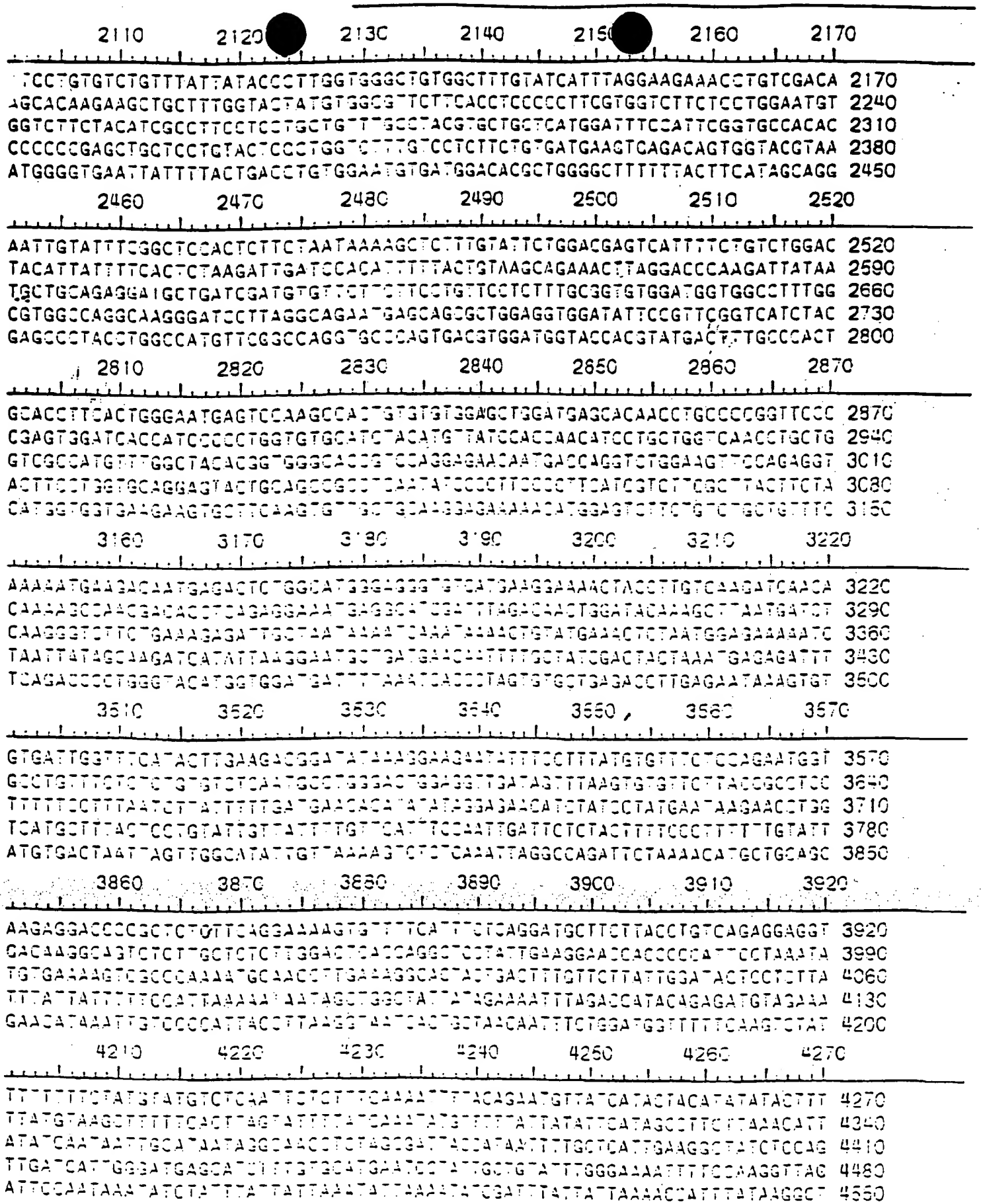
Fig. 12A (1)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2460 2470 2480 2490 2500 2510 2520
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2810 2820 2830 2840 2850 2860 2870
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3160 3170 3180 3190 3200 3210 3220
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3510 3520 3530 3540 3550 3560 3570
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3860 3870 3880 3890 3900 3910 3920
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Fig. 12A(2)

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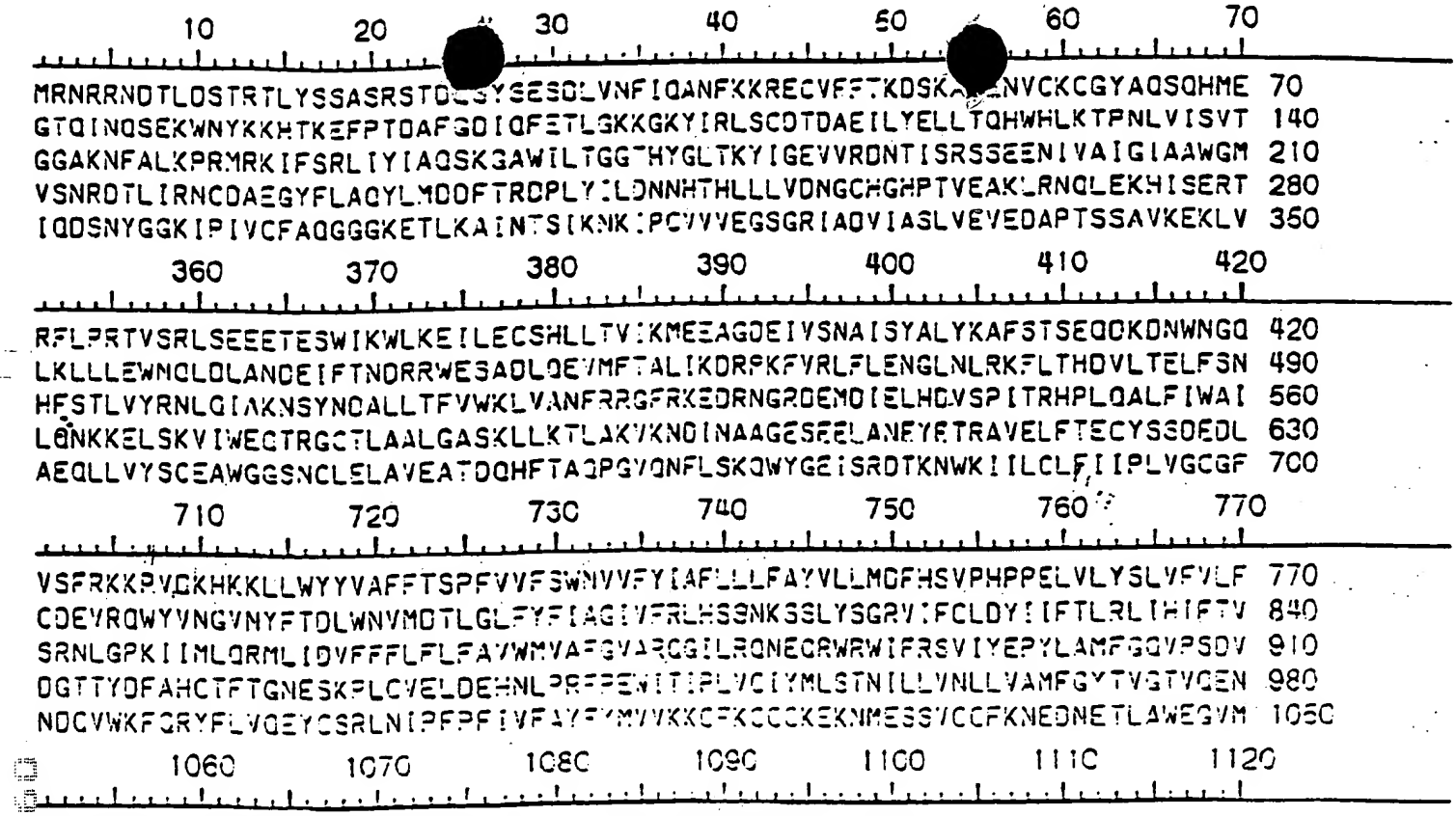
```

Fig. 12A(3)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VSNRDTLIRNCDAEGYFLAQYLMDDFTRDPLYILDNNHTHLLLVDNGCHGHPTVEAKLRNQLEKHISERT 280
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360 370 380 390 400 410 420
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Fig. 12B